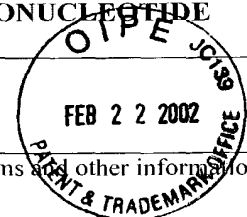
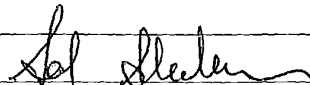
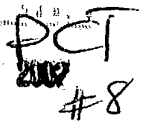


JC10 Rec'd PCT/PTO 22 FEB 2002

FORM PTO-1390(modified) U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE (REV 10-95)		ATTORNEY'S DOCKET NUMBER 02/23375
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C., 371		U.S. APPLICATION NO. (IF KNOWN), SEE 37 CFR 10/069236
INTERNATIONAL APPLICATION NO. PCT/IL00/00515	INTERNATIONAL FILING DATE 29 AUGUST 2000	PRIORITY DATE CLAIMED 1 SEPTEMBER 1999
TITLE OF INVENTION TEMPLATE-DEPENDENT NUCLEIC ACID POLYMERIZATION USING OLIGONUCLEOTIDE TRIPHOSPHATES BUILDING BLOCKS		
APPLICANT(S) FOR DO/EO/US 1) Hadar KLESS		
Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:		
<ol style="list-style-type: none"> 1. <input checked="" type="checkbox"/> This is a FIRST submission of items concerning a filing under 35 U.S.C. 371. 2. <input type="checkbox"/> This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371 3. <input checked="" type="checkbox"/> This is an express request to begin national examination procedures (35 U.S.C. 371(f) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1). 4. <input checked="" type="checkbox"/> A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date. 5. <input checked="" type="checkbox"/> A copy of the International Application as filed (35 U.S.C. 371(3)(2) <ol style="list-style-type: none"> a. <input checked="" type="checkbox"/> is transmitted herewith (required only if not transmitted by the International Bureau). b. <input checked="" type="checkbox"/> has been transmitted by the International Bureau. c. <input type="checkbox"/> is not required, as the application was filed in the United States Receiving Office (RO/US). 6. <input type="checkbox"/> A translation of the International Application into English (35 U.S.C. 371(3)(2). 7. <input checked="" type="checkbox"/> A copy of the International Search Report (PCT/ISA/210). 8. <input type="checkbox"/> Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3) <ol style="list-style-type: none"> a. <input type="checkbox"/> are transmitted herewith (required only if not transmitted by the International Bureau). b. <input type="checkbox"/> have been transmitted by the International Bureau. c. <input type="checkbox"/> have not been made; however, the time limit for making such amendments has NOT expired. d. <input type="checkbox"/> have not been made and will not be made. 9. <input type="checkbox"/> A translation of the amendments to the claims under PCT Article 19(35 U.S.C. 371(c)(3)). 10. <input checked="" type="checkbox"/> An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)). 11. <input checked="" type="checkbox"/> A copy of the International Preliminary Examination Report (PCT/IPEA/409). 12. <input type="checkbox"/> A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)). <p>Items 13 to 18 below concern document(s) of information included:</p> <ol style="list-style-type: none"> 13. <input type="checkbox"/> An Information Disclosure Statement under 37 CFR 1.97 and 1.98. 14. <input checked="" type="checkbox"/> An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included. 15. <input type="checkbox"/> A FIRST preliminary amendment. A SECOND or SUBSEQUENT preliminary amendment. 16. <input type="checkbox"/> A substitute specification. 17. <input type="checkbox"/> A change of power of attorney and/or address letter. 18. <input type="checkbox"/> Certificate of Mailing by Express Mail 19. <input type="checkbox"/> Sequence Listing Statement: The sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing. 20. <input type="checkbox"/> Other items or information: 		



U.S. APPLICATION NO. (IF KNOWN) See 37 CFR 1.01(a) 10/069236		INTERNATIONAL APPLICATION NO. PCT/IL00/00515		ATTORNEY'S DOCKET NUMBER 02/23375	
20. The following fees are submitted: BASIC NATIONAL FEE (37 CFR 1.492(a) (1) - (5)): <input type="checkbox"/> Search Report has been prepared by the EPO or JPO \$ 890 <input checked="" type="checkbox"/> International preliminary examination fee paid to USPTO (37 CFR 1.482) \$ 710 <input type="checkbox"/> No international preliminary examination fee paid to USPTO (37 CFR 1.482) but international search fee paid to USPTO (37 CFR 1.445(a)(2)) \$ 740 <input type="checkbox"/> Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO \$ 1040 <input type="checkbox"/> International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(2)-(4) \$ 100 ENTER APPROPRIATE BASIC FEE AMOUNT =				CALCULATIONS PTO USE ONLY <div style="border-top: 1px solid black; text-align: right;">\$710.00</div>	
Surcharge of \$130.00 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(e))				\$0.00	
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE	\$0.00	
Total claims	32 - 20 =	12	x \$ 18	\$216.00	
Independent claims	20 - 3 =	17	x \$ 84	\$1,428.00	
Multiple Dependent Claims (check if applicable) <input type="checkbox"/>				\$0.00	
TOTAL OF ABOVE CALCULATIONS =				\$2,354.00	
Reduction of 1/2 for filing by small entity, if applicable. <input checked="" type="checkbox"/>				\$1,177.00	
SUBTOTAL =				\$1,177.00	
Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f))				\$0.00	
TOTAL NATIONAL FEE =				\$1,177.00	
Fee for recording the enclosed assignment (37 CFR 1.2(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31) (check if applicable) <input checked="" type="checkbox"/>				\$40.00	
TOTAL FEES ENCLOSED =				\$1,217.00	
				Amount to be refunded: \$	
				charged \$	
<input type="checkbox"/> A check in the amount of \$ _____ to cover the above fees is enclosed. <input checked="" type="checkbox"/> Please charge my Deposit Account No. 50-1407 in the amount of \$ 1,217.00 to cover the above fees. A duplicate copy of this sheet is enclosed. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any fees which may be required, or credit any overpayment to Deposit Account No. 50-1407 . A duplicate copy of this sheet is enclosed. NOTE: Where an appropriate time limit under 37CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status. SEND ALL CORRESPONDENCE TO:					
SOL SHEINBEIN G.E. EHRLICH (1995) LTD. C/O ANTHONY CASTORINA SUITE 207 2001 JEFFERSON DAVIS HIGHWAY ARLINGTON, VIRGINIA 22202, USA			<div style="text-align: center;">  SIGNATURE </div> <div style="text-align: center;"> SOL SHEINBEIN NAME </div> <div style="text-align: center;"> 25,457 REGISTRATION NUMBER </div> <div style="text-align: center;"> Feb 20, 2002 DATE </div>		



A circular stamp from the Office of Intellectual Property (OIPE). The text "OIPE" is at the top, "JCT 184" is at the top right, "DEC 17 2002" is in the center, and "PATENT & TRADEMARK OFFICE" is at the bottom.

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Attorney
Docket: 02/23375

RESPONSE TO COMMUNICATION

Sol Sheinbein
Attorney for Applicant
Registration No. 425,457

December 15, 2002

TEMPLATE-DEPENDENT NUCLEIC ACID POLYMERIZATION USING OLIGONUCLEOTIDE TRIPHOSPHATES BUILDING BLOCKS

FIELD AND BACKGROUND OF THE INVENTION

5 The present invention relates to a novel activity of template-dependent polymerases and, more particularly, to the incorporation of oligonucleotide triphosphates in a template-dependent manner onto a growing nascent oligonucleotide-3'-OH group by such polymerases, to methods exploiting the advantages of the novel activity, to compositions for implementing the methods and to compounds generated while implementing the methods. The present invention provides a novel platform technology, which can be used to develop novel nucleic acid-based applications for biotechnology and nanotechnology including, for example, pharmaceuticals, biocatalysis and diagnostics.

15 It is well recognized that nucleic acid polymers possess functional capacities. These qualities may be exemplified *in vivo* as specific recognition of tRNA anticodons during translation, and by splicing activity of ribozymes. *In vitro*, several systems have been established from which functional nucleic acid polymers can be isolated. These methods of *in-vitro* evolution, termed hereinafter the directed evolution approach, include SELEX (systematic evolution of ligands by exponential enrichment) of RNA (Beaudry & Joyce, 1992) and DNA (Breaker & Joyce, 1994), and iterative use of combinatorial libraries of oligonucleotides (Frank, 1995).

25 In spite of their poor number of functional groups (*i.e.*, four bases in natural nucleotides), nucleic acid polymers may yield diverse activities such as specific binding affinity to a target molecule or catalysis of chemical-bonds formation. Recently, the inclusion of nucleotide analogs bearing alternative combination of functional groups further extend the vocabulary of nucleic acids, and establish enzymatic approaches for directed evolution as efficient technologies for isolation of functional polymers (Eaton, 1997; Benner *et al.*, 1998; Earnshaw & Gait, 1998).

35 Naturally-occurring nucleic acid polymers (DNA and RNA) maintain their basic information in the sequence order and combination of four distinct nucleotides, identified by their nitrogenous base moieties adenine and guanine, which are purine derivatives, and cytosine and thymidine (for DNA) or uracil (for RNA), which are pyrimidine derivatives (see Figure 1).

Information transfer (*e.g.*, DNA-dependent DNA replication, DNA-dependent RNA transcription, RNA-dependent DNA reverse transcription and RNA-dependent RNA replication) is performed enzymatically by mirror

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Assume, for example, the sole use of dinucleotide triphosphates as building blocks for a template-dependent synthesis of a nucleic acid molecule. Sixteen (2^4) different dinucleotide triphosphates are available for such synthesis, which represent all of the possible combinations of the four natural nucleotide monomers arranged as dimers. The 16 available dinucleotide triphosphates are: AA-triphosphate (SEQ ID NO:1); AC-triphosphate (SEQ ID NO:2); AG-triphosphate (SEQ ID NO:3); AT-triphosphate (SEQ ID NO:4); CA-triphosphate (SEQ ID NO:5); CC-triphosphate (SEQ ID NO:6); CG-triphosphate (SEQ ID NO:7); CT-triphosphate (SEQ ID NO:8); GA-triphosphate (SEQ ID NO:9); GC-triphosphate (SEQ ID NO:10); GG-triphosphate (SEQ ID NO:11); GT-triphosphate (SEQ ID NO:12); TA-triphosphate (SEQ ID NO:13); TC-triphosphate (SEQ ID NO:14); TG-triphosphate (SEQ ID NO:15); and TT-triphosphate (SEQ ID NO:16).

Further assume that unique functional groups are attached to some or all of the dinucleotide triphosphates building blocks. In this case, a polymer can be synthesized having a maximum of 16 available and precisely locatable types of functional groups, instead of a maximum of only four such groups. It will be appreciated that the maximal number of unique and precisely locatable functional groups depends on the number of monomers employed per oligonucleotide triphosphate. This maximal number equals 4^N , where N is the number of monomers per oligonucleotide triphosphate.

Therefore, the use of oligonucleotide triphosphates by template-dependent polymerases, instead of, or in addition to, nucleotide triphosphates as basic building blocks or units for template-dependent synthesis, makes possible the creation of highly complex polymers having precisely locatable functional groups.

Furthermore, if the use of oligonucleotides as building blocks for nucleic acid synthesis will become feasible, it will be appreciated that each building block becomes scarcer as compared to the use of nucleotide triphosphates. This phenomenon increases with length (N) of the oligonucleotides employed. Thus, assuming equal representation for each of the four nucleotides in a given nucleic acid polymer, a particular mononucleotide is expected, statistically, every 4 nucleotides in this polymer, a dinucleotide is expected every 16 nucleotides, a trinucleotide every 64 nucleotides (see Table 1, below), a tetranucleotide every 256 nucleotides, a pentanucleotide every 625 nucleotides, and an oligonucleotide of N-mer is expected every 4^N nucleotides, in the nucleic acid polymer. Consequently, while using relatively short

oligonucleotide sequences as building blocks for template-dependent nucleic acid synthesis, not only the total number of building blocks required for synthesizing a given nucleic acid sequence is reduced, but also each building block is less represented. As is further exemplified below, this feature can be advantageously exploited in detection of nucleic acid sequences and related applications through template-dependent polymerization.

TABLE 1

Nucleotide trimers can be arranged in 64 distinct combinations (SEQ ID NOs: 17-80, from left to right, top to bottom)

AAA	AAC	AAG	AAT	ACA	ACC	ACG	ACT	AGA	AGC	AGG	AGT	ATA	ATC	ATG	ATT
CAA	CAC	CAG	CAT	CCA	CCC	CCG	CCT	CGA	CGC	CGG	CGT	CTA	CTC	CTG	CTT
GAA	GAC	GAG	GAT	GCA	GCC	GCG	GCT	GGA	GGC	GGG	GGT	GTA	GTC	GTG	GTT
TAA	TAC	TAG	TAT	TCA	TCC	TCG	TCT	TGA	TGC	TGG	TGT	TTA	TTC	TTG	TTT

Previously, dinucleotides were indicated to be involved in initiation of transcription by RNA polymerase (Shaw *et al.*, 1980), or as building-block units in assembly of oligonucleotide through non-enzymatic means (Leberton *et al.*, 1993; Ordoukhanian & Taylor, 1997; Schmidt *et al.*, 1997). In addition, modified dinucleotides have been used as inhibitors of various viral enzymes such as reverse transcriptase (Jahnke *et al.*, 1995; Jahnke *et al.*, 1997) and integrase (Taktakishvili *et al.*, 2000). However, dinucleotide triphosphates and oligonucleotide triphosphates have not been shown to be involved, to our knowledge, in relation with template-dependent enzymatic polymerization of nucleic acids.

Therefore, there is a widely recognized need for, and it would be highly advantageous to have, methods for better exploiting the information transfer capabilities of nucleic acids (Schmidt *et al.*, 1997; Koppitz *et al.*, 1998; Ogawa *et al.*, 2000), which can serve as a platform technology for development of molecules with novel biological activities, and for the development of novel nucleic acid amplification and identification schemes. Other applications and advantages of these methods will become apparent to those of skills in the art while reading the following sections of the specification.

SUMMARY OF THE INVENTION

One object of the present invention is to develop a new approach to augment both information transfer and functional potential of nucleic acid polymers. According to this novel approach, using oligonucleotide triphosphates as building blocks for template-dependent synthesis of nucleic acids, either *per se*, or in combination with distinct chemical modifications for the introduction of functional groups in each or some of these oligonucleotides, it is possible to extend the information vocabulary and functional diversity of the polymer in a manner that is correlated to the number (N) of nucleotide units in each oligonucleotide triphosphate.

Another object of the present invention is to develop nucleic acid libraries and functional nucleic acid polymers of unprecedented complexity.

Still another object of the present invention is to develop template-dependent polymerases capable of efficiently exploiting oligonucleotide triphosphates for template-dependent synthesis of nucleic acids.

Yet another object of the present invention is to develop new approaches for template-dependent amplification of nucleic acids.

Yet another object of the present invention is to develop new approaches for nucleic acid-based diagnosis.

Yet another object of the present invention is to develop new approaches for nucleic acid-based chip technology and nanotechnology.

Yet another object of the present invention is to develop new approaches for directed evolution of nucleic acids and polypeptides.

Further and specific objects of the invention include, but are not limited to: (i) the introduction of a novel use of a template-dependent polymerase for incorporating oligonucleotide triphosphates onto a nascent oligonucleotide-3'-OH in a template-dependent manner; (ii) the development of methods for identifying a template-dependent polymerase having increased activity in incorporating oligonucleotide triphosphates onto a nascent oligonucleotide-3'-OH in a template-dependent manner; (iii) the development of methods for assaying a template-dependent polymerase for its activity in incorporating oligonucleotide triphosphates onto a nascent oligonucleotide-3'-OH in a template-dependent manner; (iv) the development of methods for better exploiting the information transfer capacity of nucleic acid molecules; (v) the development of methods for extending a nascent oligonucleotide-3'-OH in a template-dependent manner; (vi) the development of methods for amplifying nucleic acid templates; (vii) the development of methods for exponentially

amplifying nucleic acid templates; (viii) the development of methods for detecting a sequence alteration in nucleic acid templates; (ix) the development of methods for detecting the presence or absence of a sequence alteration in nucleic acid templates; (x) the development of methods for determining a sequence of a nucleic acid template; (xi) the development of nucleic acid libraries and functional nucleic acid polymers of unprecedented complexity; (xii) the development of methods for directed evolution of nucleic acids and polypeptides, (xiii) the development of methods for nucleic acid-based chip technology and nanotechnology, and (xiv) the development of compositions for effecting the above methods.

All and any objects of the present invention as stated above are made possible by a novel use of a template-dependent polymerase, the novel use comprising the step of employing the template-dependent polymerase for incorporating at least one oligonucleotide triphosphate onto a nascent oligonucleotide-3'-OH in a template-dependent manner.

According to further features in preferred embodiments of the invention described below, the template-dependent polymerase is selected from the group consisting of DNA-dependent DNA polymerase, DNA-dependent RNA polymerase, RNA-dependent DNA polymerase and RNA-dependent RNA polymerase.

According to still further features in the described preferred embodiments the template-dependent polymerase is thermostable.

According to another aspect of the present invention there is provided a composition or a plurality of compositions comprising 4^N oligonucleotide triphosphates each having N monomers, wherein N is an integer greater than 1.

According to still another aspect of the present invention there is provided a composition comprising at least one oligonucleotide triphosphate and at least one nucleotide triphosphate, wherein the at least one oligonucleotide triphosphate and the at least one nucleotide triphosphate are selected such that monomers forming the at least one oligonucleotide triphosphate are not represented among the at least one nucleotide triphosphate and vice versa.

According to further features in preferred embodiments of the invention described below, each of the oligonucleotide triphosphates includes at least two monomers. The number of nucleotide units is preferably up to six, but it may be higher.

According to one preferred embodiment of the invention, the at least one oligonucleotide triphosphate is unmodified with respect to the natural base, sugar, and/or phosphate residues.

According to still further features in the described preferred embodiments, at least one of the oligonucleotide triphosphates is chemically modified in the natural residues of the base, sugar and/or phosphate or any other internucleosidyl linkage.

The present invention successfully addresses the shortcomings of the presently known configurations of nucleic acids as information messengers by exploiting a novel activity of template-dependent polymerases, *i.e.*, their ability to incorporate, in a template-dependent manner, an oligonucleotide triphosphate to a growing 3'-OH group, thereby better exploiting the information transfer capacity of nucleic acids.

15 BRIEF DESCRIPTION OF THE DRAWINGS

The invention is herein described, by way of example only, with reference to the accompanying drawings, wherein:

FIG. 1 shows the general formula of the natural 2'-deoxynucleoside wherein Base is one of the four natural bases illustrated in the figure.

20 FIG. 2 illustrates the chemical makeup of the thymidylyl-3'-5'-thymidine dinucleotide triphosphate form, TpT3p (SEQ ID NO:16).

FIG. 3 is a schematic representation of the polymerization assay for detecting incorporation of a dinucleotide triphosphate. Step I: primer extension using primer T7, template T1, DNA polymerase and the deoxynucleotides dATP, dCTP and dGTP in the presence (left) or absence (right) of TpT3P. Step II: treatment of the products from the previous step with *Exo* VII to eliminate ss-DNA regions. Step III: PCR amplification of the products from the previous step using primers T7 and B, and a connecting fragment, T2, that overlaps with the extended portion of T1 (bold line). This portion of T1 contains a run of 3, 4 or 5 A's (in oligonucleotides T1-3, T1-4 and T1-5, respectively; see Table 2), flanked (on its 5' side) by a non-A containing region. PCR amplification in step III will occur only if the extension proceeded to the end of T1 on step I.

35 FIG. 4 shows photographs of agarose gels that illustrate the polymerization assay using the templates T1-4, T1-3 or T1-5 (see Table 2). The reactions in step I (lanes a-e) contained; a: all four dNTP's; b: no dNTP's; c: dATP, dCTP and dGTP; d: as in c, but with 3 μ M of TpT3p, e: no T1 template; f-g: PCR of step III with and without T1 template, respectively.

FIG. 5 provides an example of implementing the present invention for distinguishing between gene sequences of a wild type (*A*, SEQ ID NO:87) and a mutant (*B*, SEQ ID NO:88) containing a single point mutation (T to G, underlined). The sequences can be replicated from a specific primer at the 5' end (not shown) using the two given sets of dinucleotide combinations and a DNA polymerase. Set I supports complete amplification of *A*, but not of *B* due to the presence and absence of the dinucleotides AC and CC, respectively. Accordingly, set II is suitable only for the amplification of sequence *B* but not of *A*. The amplified products can be separated from the reaction to indicate which sequence, wild type, mutant or both, are present.

FIG. 6 shows an assay of labeled-primer extension demonstrating incorporation of the dinucleotide triphosphates TpT3p and CpA3p in a template-dependent manner onto a 3' end of a primer. The reactions includes labeled primer p201 (SEQ ID NO:92) and templates T80 (SEQ ID NO:93) (lanes 1-4), and T81 (SEQ ID NO:94) (lanes 5-7). The nucleotides content in these reactions is: none (lane 1), all 4 dNTP's (lane 2), CpA3p (lanes 3 and 5), CpA3p and TpT3p (lanes 4, 6 and 7). The reaction in lane 7 contains two fold the concentration of dinucleotides as is compared to that of lane 6.

FIG. 7 shows an assay of labeled-primer extension demonstrating incorporation of di- and trinucleotide triphosphates in a template-dependent manner onto a 3' end of a primer. The reactions include labeled primer p201 (SEQ ID NO:92) and template T24 (SEQ ID NO:96). The nucleotide content in these reactions is: none (lane 1), all 4 dNTP's (lane 2), dCTP and dATP (lane 3), dCTP, dATP and TpT3p (lane 4), dCTP, dATP and TpTpT3p (lane 5), CpA3p (lane 6), and CpC3p (lane 7).

FIG. 8 shows an assay of labeled-primer extension demonstrating template-dependent incorporation of ApG3p and TpC3p dinucleotides. The reactions include labeled primer p201 (SEQ ID NO:92) and template T83 (SEQ ID NO:95). The nucleotide content in these reactions is: all 4 dNTP's (lane 1) and ApG3p and TpC3p dinucleotides (lane 2).

DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention is of (i) a novel use of a template-dependent polymerase for incorporating oligonucleotide triphosphates onto a nascent oligonucleotide-3'-OH in a template-dependent manner; (ii) methods for identifying a template-dependent polymerase having increased activity in incorporating oligonucleotide triphosphates onto a nascent oligonucleotide-3'-

OH in a template-dependent manner; (iii) methods for assaying a template-dependent polymerase for its activity in incorporating oligonucleotide triphosphates onto a nascent oligonucleotide-3'-OH in a template-dependent manner; (iv) methods for better exploiting the information transfer capacity of a nucleic acid molecule; (v) methods for extending a nascent oligonucleotide-3'-OH in a template-dependent manner; (vi) methods for amplifying a nucleic acid template; (vii) methods for exponentially amplifying a nucleic acid template; (viii) methods for detecting a sequence alteration in a nucleic acid template; (ix) methods for detecting the presence or absence of a sequence alteration in a nucleic acid template; (x) methods for determining a sequence of a nucleic acid template; (xi) nucleic acid libraries and functional nucleic acid polymers of unprecedented complexity and functional space; (xii) methods for directed evolution of nucleic acids and polypeptides; (xiii) methods for nucleic acid-based chip technology and nanotechnology, and (xiv) compositions for effecting the above methods.

20 The principles and operation of the present invention may be better understood with reference to the drawings and accompanying descriptions.

According to one aspect of the present invention there is provided a novel use of a template-dependent polymerase. The novel use, according to this aspect of the present invention, comprises the step of employing the template-dependent polymerase for incorporating at least one oligonucleotide triphosphate onto a nascent oligonucleotide-3'-OH in a template-dependent manner.

As used herein in the specification and in the claims section that follows, the phrases "oligonucleotide triphosphate" or in plural "oligonucleotide triphosphates" include single-stranded chains of at least two nucleotides connected via 3' -> 5' internucleosidyl linkages, and which have a triphosphate group attached to the 5' end of the first nucleotide as illustrated in Figure 2.

As used herein in the specification and in the claims section that follows, the terms "nucleotide" or in plural "nucleotides" which are interchangeably used with the terms "monomer" or in plural "monomers" include native (naturally occurring) nucleotides, which include a nitrogenous base selected from the group consisting of adenine, thymidine, cytosine, guanine and uracil, a sugar selected from the group of ribose and deoxyribose (the combination of the base and the sugar is known as nucleoside), and one to three phosphate groups, and which can form phosphodiester internucleosidyl linkages. However, these terms, as used herein, further include nucleotide analogs. Such analogs can have a sugar analog, a base analog and/or an internucleosidyl linkage analog. In addition, analogs exhibiting non-standard base pairing, such as described in, for example, U.S. Pat. No. 5,432,272, which is incorporated herein by reference, is also included under these terms. Thus, as used herein these terms read on molecules capable of, while incorporated in a polymer, conventional or unconventional pairing via hydrogen bonding with naturally occurring nucleotides or with nucleotide analogs exhibiting non standard base pairing and which are present in a complementary polymer.

25 As used herein in the specifications and in the claims section that follows, the term "nucleotide analog" includes nucleotides that are chemically modified in the natural base (hereinafter "base analogs"), in the natural sugar (hereinafter "sugar analogs"), and/or in the natural phosphodiester or any other internucleosidyl linkage (hereinafter "internucleosidyl linkage analogs").

30 The nucleotide analogs of the invention may bear at least one functional group selected from: (i) a chemically-reactive group being a group involved in formation or cleavage of any form of a chemical interaction involving electron, proton, or charge transfer including, but not being limited to, a nucleophile, a hydrogen-bond donor, a hydrogen-bond acceptor, an acid, a base, a charged moiety, a hydrophilic moiety, a metal ligand, and a leaving group; (ii) a
35 chemically-inert group being a group involved in interactions that have no electron, proton, or charge transfer, but that may have a structural role,

including, but not being limited to, a hydrophobic moiety; (iii) a cross-linking group; (iv) a labeling group, and (v) a first binding-group of a binding pair, which are related to each other by specific binding affinity.

5 The functional group as above may be linked directly to the base, sugar, or internucleosidyl linkage, or through a spacer, so as to reduce steric hindrance that may interfere with binding to the polymerase and/or with pairing to the template.

It will be appreciated that a variety of functional groups have been successfully bound to nucleotides. It will further be appreciated that such binding did not hamper the ability of template-dependent polymerases to employ nucleotides derivatized by such functional groups as building blocks for template-dependent nucleic acid synthesis.

A first binding group of a binding pair can be any member of a binding pair, such as, but not limited to, biotin-avidin/streptavidin, ligand-receptor, antigen/hapten-antibody, magnetized bead-magnet/electromagnet, substrate analog-enzyme, metal ion-chelator, and the like. The first binding group of the binding pair is preferably selected the smaller one, so as to minimize steric hindrance. In the listed examples, the smaller binding pairs are biotin of the biotin-avidin/streptavidin pair, ligand of the ligand-receptor pair, antigen/hapten of the antigen/hapten (*e.g.*, digoxigenin)-antibody pair, magnetized bead of the magnetized bead-magnet/electromagnet pair, substrate analog of the substrate analog-enzyme pair, and metal ion of the metal ion-chelator pair.

It will be appreciated that a variety of binding groups, such as, but not limited to, biotin, the antigen digoxigenin and magnetized beads have been successfully bound to nucleotides. It will further be appreciated that such binding did not hamper the ability of template-dependent polymerases to employ nucleotides derivatized by binding groups as building blocks for template-dependent synthesis of nucleic acids.

30 A cross-linking group is a reactive group capable of covalently bonding to another group when appropriate proximity and orientation are established between the groups. A cross-linking group can be selected non-reactive unless activated by an external stimuli, such as radiation of the appropriate wavelength or wavelength range or a chemical. Examples of cross-linking groups which
35 can be bound to a nucleotide include, but are not limited to brominated and iodinated nucleotides such as 5'-bromodeoxyuridine, 8'-bromodeoxyadenosine and 5'-iododeoxycytidine, or thiol-containing nucleotides such as 6'-

Examples of base analogs that can be used according to the invention include, but are not limited to, modified purine and pyrimidine bases such as, for example, O-methyl, C-methyl, N-methyl, deaza, aza, halo (F, Br, I), thio, oxo, aminopropenyl, amino, acyl, propynyl, pentynyl, and etheno base derivatives, as well as more drastic modifications such as replacement of the base by phenyl and even complete deletion of the base (abasic), and additional analogs as described in Eaton, (1997); Benner *et al.*, (1998); Earnshaw & Gait, (1998) and Sakthivel & Barbas (1998).

Examples of sugar analogs that can be used according to the invention include, but are not limited to, modifications of the β -ribofuranosyl and β -2'-deoxyribofuranosyl sugar residues such as, for example, 2'-O-methyl, 2'-O-allyl, 2'-O-amino, 2'-deoxy-2'-halo (F, Cl, Br, I), 2'-deoxy-2'-thio, 2'-deoxy-2'-amino and dideoxy derivatives, as well as corresponding α -anomers and hexose analogs, and additional analogs as described in Eaton, (1997); Benner *et al.*, (1998); Earnshaw & Gait, (1998); Groebke *et al.*, (19) and Sakthivel & Barbas (1998).

Examples of internucleosidyl analogs that can be used according to the invention include, but are not limited to, those in which the natural phosphodiester linkage is replaced by a linkage such as phosphorothioate, phosphorodithioate, phosphoroamidate, methylphosphonate, and additional analogs as described in Eaton, (1997); Benner *et al.*, (1998); Earnshaw & Gait, (1998) and Sakthivel & Barbas (1998).

Also can be used peptide nucleic acids (PNA), in which the entire phosphate-sugar backbone is replaced with a backbone consisting of (2-aminoethyl) glycine units to which bases are attached through methylenecarbonyl bridges.

As used herein in the specification and in the claims section that follows, the phrases "template-dependent manner" or "template-dependent synthesis of nucleic acids " refer to successive polymerization of oligonucleotide triphosphates or of oligonucleotide triphosphates and nucleotide triphosphates in a fashion dictated by the sequence order of a complementary template.

In order to better suit the applications proposed herein for the present invention, the polymerization activities of template-dependent polymerases are preferably improved in terms of efficiency and specificity. This can be achieved by modifying certain protein components involved in the catalytic activity of such polymerases.

The chemistry involves attack of the 5'- α -phosphate of the incoming nucleotide on the 3'-OH group of the end terminal nucleotide of the nascent oligonucleotide, which is deprotonated via the metal ions. This is accompanied by hydrolysis of the triphosphate, release of a pyrophosphate and formation of a phosphodiester bond that extends the primer by one nucleotide at a time.

Protein modifications could conceivably include, but are not limited to, replacements, deletions and insertions of amino acid residues in specific or random locations of the enzyme. As it is presently impractical to anticipate in advance which amino acid modifications will be responsible for functional adjustment, a semi-rational approach for engineering the polymerase is envisioned. Based on the crystal structure available for the large fragment of, for example, Taq DNA polymerase (Li *et al.*, 1998) and other polymerases (Singh & Modak, 1998; Doubli *et al.*, 1999), a set of enzyme domains are chosen for modifications. For example, such domains in Taq DNA polymerase include the O helix of the fingers region (Li *et al.*, 1998; Morales & Kool, 1999). Modifications are introduced into the corresponding gene regions which are cloned in suitable expression vectors by, for example, directed evolution means involving random point-mutations in the chosen domain regions, random shuffling of fragments of part or the whole gene, and family shuffling of genes having similar sequences (Stemmer, 1994; Cramer *et al.*, 1998; Zhao *et al.*, 1998; Minshull & Stemmer, 1999). These generate a library of polymerase genes expressing many different "versions" of the original enzyme, of which

The main functional goal for polymerase modifications is to improve catalytic efficiency of template-dependent incorporation of oligonucleotide triphosphates. This is the basis for selecting the most proficient enzymes from the diverged library. Proteins expressed from the library are divided into several batches, which are used in a polymerase selection-assay that is further described below. In one step of this assay, the concentration of the appropriate nucleotide units and the reaction time are monitored to select for the best enzyme variants. Chosen clones are further modified by consecutive iterations of the same engineering approach until the desired efficiency is reached.

Therefore, according to yet another aspect of the present invention there is provided a method of identifying a template-dependent polymerase having increased activity in incorporating oligonucleotide triphosphates onto a nascent oligonucleotide-3'-OH in a template-dependent manner, the method comprising implementation of the following method steps, of which, in a first step, a library of mutated template-dependent polymerases is constructed.

Such construction can be effected, for example, by mutating (e.g., randomly mutating) a gene encoding the template-dependent polymerase by nucleotide alteration, deletion, addition, shuffling, *etc.*, to obtain a repertoire of mutated template-dependent polymerases genes which encode a repertoire of mutated template-dependent polymerases. Such polymerases can then be expressed by, for example, bacteria or eukaryotic cells, by methods known in the art. In a second step of the method according to this aspect of the present invention, the library, of proteins of individual clones or of pooled clones is screened using template-dependent polymerization of oligonucleotide triphosphates for selecting a template-dependent polymerase mutant exhibiting

increased activity in incorporating the oligonucleotide triphosphates onto the nascent oligonucleotide-3'-OH in a template-dependent manner.

An assay for template-dependent polymerization of oligonucleotide triphosphates can be effected in any one of a plurality of ways. The Examples section that follows demonstrate template-dependent polymerization of oligonucleotide triphosphates that can be used with individual or pooled protein extracts, and with purified or partially purified mutant polymerases.

Once a template-dependent polymerase mutant exhibiting increased activity in incorporating oligonucleotide triphosphates onto a nascent oligonucleotide-3'-OH in a template-dependent manner is identified, such a polymerase may serve for a second round of mutating and screening as described above.

Thus, according to a preferred embodiment of this aspect of the present invention, the method is further effected and polished by using the template-dependent polymerase mutant identified above as a basis for creating a second library of mutated template-dependent polymerases derived therefrom and screening the second library using template-dependent polymerization of oligonucleotide triphosphates for selecting a second template-dependent polymerase mutant demonstrating yet increased activity in incorporating the oligonucleotide triphosphates onto the nascent oligonucleotide-3'-OH in a template-dependent manner.

According to still further features in the described preferred embodiments the library of mutated template-dependent polymerases is created using random mutagenesis, random fragments shuffling and/or gene-family shuffling of genes corresponding to protein fragments and/or domains.

According to an additional aspect of the present invention there is provided a method of assaying a template-dependent polymerase for its activity in incorporating oligonucleotide triphosphates onto a nascent oligonucleotide-3'-OH in a template-dependent manner, the method comprising the step of using template-dependent polymerization of oligonucleotide triphosphates for assaying the template-dependent polymerase for its activity in incorporating oligonucleotide triphosphates onto the nascent oligonucleotide-3'-OH in a template-dependent manner.

Oligonucleotide triphosphates may be mixed into compositions, which are useful in implementing the methods of the present invention as are further described below.

Thus, according to another aspect of the present invention there is provided a composition or a plurality of individually packed compositions forming a kit comprising 4^N oligonucleotide triphosphates each having N monomers in a single mix or any combination of sub-mixes, wherein N is an integer greater than 1.

Thus, if N equals 2 (dinucleotide), 16 different oligonucleotide triphosphates are included in the single mix or any combination of the sub-mixes; if N equals 3 (trinucleotide), 64 different oligonucleotide triphosphates are included in the single mix or any combination of the sub-mixes; if N equals 4 (tetranucleotide), 256 different oligonucleotide triphosphates are included in the single mix or any combination of the sub-mixes; if N equals 5 (pentanucleotide), 1024 different oligonucleotide triphosphates are included in the single mix or any combination of the sub-mixes; whereas if N equals 6 (hexanucleotide), 4096 different oligonucleotide triphosphates are included in the single mix or any combination of the sub-mixes; and so on.

However, compositions according to the present invention may include oligonucleotide triphosphates and also combinations of oligonucleotide triphosphates and nucleotide triphosphates.

Of particular interest are compositions including at least one oligonucleotide triphosphate and at least one nucleotide triphosphate, wherein the at least one oligonucleotide triphosphate and the at least one nucleotide triphosphate are selected such that monomers forming the at least one oligonucleotide triphosphate are not represented among the at least one nucleotide triphosphate and *vice versa*. As further detailed below, such compositions may find use in, for example detection of sequence alterations in a nucleic acid template.

Oligonucleotide triphosphates may be attached on a solid support, which are useful in implementing the methods of the present invention as are further described below.

Thus, according to another aspect of the present invention there is provided a setup, in which at least one of the oligonucleotide triphosphates, used for template-dependent polymerization, is attached onto a solid support as part of, for example, a nanodevice or a DNA chip.

The following provides detailed description of some methods, which can find uses in pharmaceuticals, biocatalysis, diagnostics, and nanotechnology according to the present invention.

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According to yet an additional aspect of the present invention there is provided yet an additional method of detecting a sequence alteration in a nucleic acid template, the method comprising the step of contacting the nascent oligonucleotide-3'-OH with a nucleic acid template, a template-dependent polymerase, at least one oligonucleotide triphosphate and at least one nucleotide triphosphate, wherein the at least one oligonucleotide triphosphate and the at least one nucleotide triphosphate are selected such that at least one monomer of the at least one oligonucleotide triphosphate is absent from the at least one nucleotide triphosphate, under conditions in which the nascent oligonucleotide-3'-OH hybridizes with the nucleic acid template and the template-dependent polymerase is active in incorporating the at least one oligonucleotide triphosphate onto the 3'-OH group of the nascent oligonucleotide-3'-OH, thereby extending the nascent oligonucleotide-3'-OH in the template-dependent manner, wherein the at least one oligonucleotide triphosphate is selected so as to enable extending the nascent oligonucleotide-3'-OH in the template-dependent manner only if the sequence alteration is present, or in the alternative, only if the sequence alteration is absent.

According to still an additional aspect of the present invention there is provided still an additional method of detecting the presence or absence of a sequence alteration in a nucleic acid template, the method comprising the steps of: (a) contacting the nucleic acid template with a nascent oligonucleotide-3'-OH, a template-dependent polymerase and at least one oligonucleotide triphosphate under conditions in which the nascent oligonucleotide-3'-OH hybridizes with the nucleic acid template and the template-dependent polymerase is active in incorporating the at least one oligonucleotide triphosphate onto a growing 3'-OH group of the nascent oligonucleotide-3'-OH if appropriate base pairing exists between the nucleic acid template and the oligonucleotide triphosphate, and the template-dependent polymerase is substantially inactive in incorporating the at least one oligonucleotide triphosphate onto the growing 3'-OH group of the nascent oligonucleotide-3'-OH if appropriate base pairing fails to exist between the nucleic acid template and the at least one oligonucleotide triphosphate; and (b) detecting whether the at least one oligonucleotide triphosphate is incorporated onto the growing 3'-OH group of the nascent oligonucleotide-3'-OH, thereby detecting the presence or absence of the sequence alteration in the nucleic acid template.

According to a further aspect of the present invention there is provided a further method of detecting the presence or absence of a sequence alteration in a nucleic acid template, the method comprising the steps of: (a) contacting the nucleic acid template with a nascent oligonucleotide-3'-OH, a template-dependent polymerase, at least one oligonucleotide triphosphate and at least one nucleotide triphosphate, wherein the at least one oligonucleotide triphosphate and the at least one nucleotide triphosphate are selected such that at least one monomer of the at least one oligonucleotide triphosphate is absent from the at least one nucleotide triphosphate, under conditions in which the nascent oligonucleotide-3'-OH hybridizes with the nucleic acid template and the template-dependent polymerase is active in incorporating the at least one oligonucleotide triphosphate and the at least one nucleotide triphosphate onto a growing 3'-OH group of the nascent oligonucleotide-3'-OH if appropriate base pairing exists between the nucleic acid template and the at least one oligonucleotide triphosphate, and the template-dependent polymerase is substantially inactive in incorporating the at least one oligonucleotide triphosphate onto the growing 3'-OH group of the nascent oligonucleotide-3'-OH if appropriate base-pairing fails to exist between the nucleic acid template and the at least one oligonucleotide triphosphate; and (b) detecting whether the oligonucleotide triphosphate is incorporated onto the growing 3'-OH group of the nascent oligonucleotide-3'-OH, thereby detecting the presence or absence of the sequence alteration in the nucleic acid template.

According to yet a further aspect of the present invention there is provided a method of determining a sequence of a nucleic acid template, the method comprising the steps of: (a) contacting in one or more reaction vessels the nucleic acid template with a nascent oligonucleotide-3'-OH, a template-dependent polymerase, 4^N oligonucleotide triphosphates each including N monomers, 4^N oligonucleotide triphosphate analogs each including N monomers of which a 3' monomer includes a chain-terminator moiety, such as a dideoxy-ribose moiety, wherein N is an integer greater than 1, under conditions in which the nascent oligonucleotide-3'-OH hybridizes with the nucleic acid template and the template-dependent polymerase is active in incorporating the oligonucleotide triphosphates and the oligonucleotide triphosphate analogs onto a growing 3'-OH group of the nascent oligonucleotide-3'-OH, so as to obtain a population of nucleic acid chains each being terminated by a different oligonucleotide triphosphate analog of the 4^N oligonucleotide triphosphate analogs; and (b) size-separating, e.g., by gel electrophoresis, the population of

terminated nucleic acid chains, thereby determining the sequence of the nucleic acid template.

Several alternative protocols can be followed to execute the above sequencing method, which protocols depend, to a great extent, on the labeling strategy employed.

Thus, if the oligonucleotide-3'-OH is labeled, two options exist. According to the first option, 4^N different labels are employed. In this case 4^N reaction mixtures are prepared each of which includes a uniquely labeled oligonucleotide-3'-OH and a corresponding unique oligonucleotide triphosphate chain-terminator. Thereafter, a single lane can be employed for electrophoretic separation of the population of nucleic acid chains. According to the second option, a single label is employed. In this case again 4^N reaction mixtures are prepared each of which includes the labeled oligonucleotide-3'-OH and a unique oligonucleotide triphosphate chain-terminator. Thereafter, 4^N lanes are employed for electrophoretic separation of the population of nucleic acid chains. It will be appreciated that a similar protocol can be adopted if a single label is employed to label the oligonucleotide triphosphates employed in the reaction.

Alternatively, if the oligonucleotide triphosphate terminators are labeled, again, two options exist. According to the first option, 4^N different labels are employed. In this case a single reaction mixture is prepared and a single lane can be employed for electrophoretic separation of the population of nucleic acid chains. According to the second option, a single label is employed. In this case again 4^N reaction mixtures are prepared and 4^N lanes are employed for electrophoretic separation.

Since 4^N according to the present invention are at least 16 and further since instrumentation capable of uniquely detecting 16 unique labels is presently not available, according to a preferred embodiment of the present invention at least some of the unique labels are combinatorial labels. Fluorescent combinatorial labels have so far been successfully employed as chromosomal paints to label each of the 24 human male chromosomes by a unique identifiable paint and may therefore serve as unique labels according to the present invention. For further detail regarding combinatorial labels the reader is referred to U.S. Pat. No. 5,871,932, which is incorporated herein by reference.

compatibility of the analogs with enzymatic polymerization. Failure to comply with enzymatic polymerization can result from interference of base pairing in the template or of interactions with the polymerase.

Using oligonucleotide triphosphates for polymerization overcome some of the above limitations. The addition of chemical groups in various base and sugar positions may be more suitable for polymerization, as base-pair interactions between the template and the incoming unit are more stable. Unique to this system, the natural connecting phosphodiester-bond between the two nucleosides is now a novel site for modifications extending flexibility and conformational space of the polymeric chain. Furthermore, the complexity of polymers synthesized from 4^N different nucleotide building blocks, is much higher than of polymers with a four-base code. For example, a 10-mer oligonucleotide of standard bases has about 10⁶ distinct possibilities, while that of dimers contain about 10¹² different combinations.

15 In screening for novel lead compounds for drug development, and for polymeric biocatalysts, combinatorial libraries of nucleic acids generated through enzymatic amplification and directed evolution are clearly superior over chemically synthesized libraries. The novel technology of the present invention further strengthens these approaches. The uncovered activity of
20 template-dependent polymerases according to the present invention can serve to generate almost any complex nucleic acid molecule due to the very high complexity of the combinatorial approach.

Thus, it enables the preparation of nucleic acid polymers having at least one functional group in at least one type of nucleotide at a pre-selected location of the polymer.

This aspect of the present invention is readily achievable using functional groups in derivatized oligonucleotide triphosphates. Consider, for example, using dinucleotide triphosphates and a modified A. There are 7 different dimers in which A is in a distinct sequence-context, and therefore one can use up to 7 different functional groups of A when polymerizing with dimers. If trinucleotide triphosphates are used, a modified A can resume any one of 37 distinct trimers (see, for example, all the A-containing trimers in Table 1), and therefore one can use up to 37 different functional groups of A when polymerizing with trimers. If oligonucleotide triphosphates of N monomers are used, a modified A can resume any one of $4^N - 3^N$ distinct sequence-context positions and therefore one can use $4^N - 3^N$ different functional groups when polymerizing with of N-mer oligonucleotides.

Furthermore, by using a mixture of two different analogs of the same type of nucleotide, the above-described complexity increases to $5^N - 3^N$. Therefore, a very large functional diversity can be introduced into a given sequence context of the template by using several different analogs of each nucleotide.

Some of the applications that can be developed based on the new technology are further described in the following paragraphs.

Nucleotide polymers with specific binding affinity or catalytic activity can be isolated from combinatorial libraries of polymers generated using the present invention. The libraries may be initially formed in the DNA sequences through mutations and shuffling by conventional means known to those skilled in the art. The sequence diversity can then be translated to sequence combinations of distinct oligonucleotide building blocks, each containing a unique functional group. The functional polymers are thereafter generated by template-dependent synthesis using a polymerase and can replace proteins in *in-vitro* applications such as specific nucleases, or create novel catalysts that are useful, for example, in organic synthesis reactions.

Large combinatorial libraries of nucleic acids have been efficiently utilized in screening of lead compounds for developing bioactive compounds such as drugs (Desai *et al.*, 1994; Fauchere *et al.*, 1998). The nucleic acid libraries generated from oligomeric units, according to the present invention, have, potentially, the highest level of complexity, which maximize the diversity and increase the chances of finding a certain bioactive compound, and are therefore more efficient for screening of lead bioactive compounds.

Specific ligands such as oligonucleotides and antibodies are used in chips for recognition and quantitation of DNA and protein molecules. Due to their higher complexity and large repertoire for generating specific ligands, the dinucleotide-based polymers may be used to rival the current molecules in DNA and protein chips.

In nanotechnology, self-assembled units need to form networks that manage information transfer and processing events in molecular scale. Functional nucleic acid polymers embody the basic features for such networks: (a) self-assembly capacity for molecular network setup; (b) addressing-locating an information point in the network by specific recognition and affinity; and (c) information processing-catalytic potential to transfer molecular changes of specific components of the network. The oligonucleotide triphosphate system for nucleic acid polymer synthesis presented herein is the first system to hold

all such qualities in one molecule, and is therefore uniquely suited to function as the basis of future "molecular software" in nanotechnology.

Thus, according to yet an additional aspect of the present invention there is provided a method of better exploiting the information transfer and functional capacities of nucleic acid molecules for DNA chip technology and nanotechnology, the method comprising the step of contacting a component selected from at least one nucleic acid template, at least one template-dependent polymerase, at least one nascent oligonucleotide-3'-OH, at least one oligonucleotide triphosphate and/or at least one oligonucleotide triphosphate analog, wherein at least one of said components is attached onto a solid support used in a nanodevice or DNA chip, and wherein said at least one template-dependent polymerase is active in incorporating said at least one oligonucleotide triphosphate and/or said at least one oligonucleotide triphosphate analog onto said growing 3'-OH group of said nascent oligonucleotide-3'-OH, so as to obtain a population of nucleic acid chains bound to the solid support, which can be further manipulated by means as described above including, but not limited to, template-dependent extension, template-dependent amplification, detection of sequence alteration, and detection of nucleic acid sequences.

The directed evolution approach revolutionized the field of nucleic acid and protein engineering. This approach is based on natural evolution strategies that link between multiplication, diversity and fitness. These strategies adopted in the directed evolution approach open enormous possibilities to engineer natural molecules *in vitro*, and to create *de novo* unnatural molecules that are useful for mankind (Stemmer, 1994; Zhao *et al.*, 1998; Minshull & Stemmer, 1999). Methods and technologies for performing these tasks are therefore valuable.

Thus, according to yet an additional aspect of the present invention there is provided a method of exploiting oligonucleotide triphosphates for engineering functional nucleic acid polymers and polypeptides by directed evolution, the method comprising the steps of: (a) contacting in reaction vessels a nucleic acid template with a nascent oligonucleotide-3'-OH, a template-dependent polymerase, and 4^N oligonucleotide triphosphates, each including N monomers, wherein N is an integer greater than 1, and wherein at least one of said oligonucleotide triphosphates has a mismatch as compared to the template sequence, under conditions in which the nascent oligonucleotide-3'-OH hybridizes with the nucleic acid template and the template-dependent

polymerase is active in incorporating said oligonucleotide triphosphates and said at least one oligonucleotide triphosphate containing said mismatch onto a growing 3'-OH group of the nascent oligonucleotide-3'-OH, so as to obtain a population of nucleic acid chains each containing one or multiple mutations; and (b) amplifying said mutated population of nucleic acid chains and further shuffling, cloning and expressing them by methods known in the art to create pools of degenerate nucleic acid sequences and of degenerate polypeptides; and (c) screening said pools for individual clones with desired properties, and then using the selected clones as precursors for additional cycles of degeneration and selection, as described above, until the selected molecules are optimized for the desired function. In this way, the nucleic acid sequences and polypeptides are engineered to acquire specific functional properties.

Additional objects, advantages, and novel features of the present invention will become apparent to one ordinarily skilled in the art upon examination of the following examples, which are not intended to be limiting. Additionally, each of the various embodiments and aspects of the present invention as delineated above and as claimed in the claims section below finds experimental support in the following examples.

EXAMPLES

Reference is now made to the following examples, which together with the above descriptions illustrate the invention in a non-limiting fashion.

Generally, the nomenclature used herein and the laboratory procedures in recombinant DNA technology described below are well known and commonly employed in the art. Standard techniques are used for cloning, DNA and RNA isolation, amplification and purification. Generally enzymatic reactions involving DNA ligase, DNA polymerase, restriction endonucleases and the like are performed according to the manufacturers' specifications. These techniques and various other techniques are generally performed according to Sambrook *et al.*, (1989), which is incorporated herein by reference. Nucleic acid chemistry is generally performed according to Gait, (1984), which is incorporated herein by reference. All of the oligonucleotides used for the polymerization assays were prepared by solid phase synthesis, and further purified by electrophoresis on Urea-PAGE. Other general references are provided throughout this document. The procedures therein are believed to be well known in the art and are provided for the convenience of the reader. All the information contained therein is incorporated herein by reference.

Example 1

Dinucleotide triphosphate preparation

Thymidylyl-3'-5'-thymidine (TpT) dinucleotide was synthesized in liquid by V. Bogachev and V. Silnikove, of the Novosibirsk Institute of Bioorganic Chemistry in Russia. TpT was converted to the triphosphate form (TpT3p, SEQ ID NO:16; Figure 2) in two steps. First, it was phosphorylated to a 5'-monophosphate form by phosphoryl chloride; then, the 5'-phosphate group was activated by N-methylimidazole and reacted with pyrophosphate (tributylammonium salt) forming the desired triphosphate (Bogachev, 1996).

Following this procedure, 15 mg of TpT-OH (27 mmol) yielded 3 mg (3.8 mmol) of purified TpT3p. The purified dinucleotide was analyzed by ³¹P-NMR (D₂O) recorded on a Bruker AC 250 spectrometer (Karlsruhe, Germany). ³¹P chemical shifts are reported in ppm relative to 80 % phosphoric acid and are positive when downfield from the reference. Spectra of four distinct peaks of the triphosphate TpT3p: delta= -10.32 (d, J= 19 Hz, P-alpha.), -22.04 (t, J= 19 Hz, P-beta.), -7.46 (d, J= 19 Hz, P-gamma), and of the phosphodiester phosphate: delta= 0.39 (s).

Example 2

Dinucleotide triphosphate purification

TpT3p was purified by two ion-exchange chromatography steps: a EMD-DEAE (Merck) column using 0.01–1.2 M LiCl gradient, and by Source 15Q PE column (Pharmacia) using 0.2–1 M NaCl gradient, buffered with 25 mM triethylamine acetate, pH 4. The dinucleotide fractions were further desalted on DEAE Sepharose (Merck) column eluted with 1M triethylamine bicarbonate (TEAB), pH 8. After evaporation and removal of the TEAB, TpT3p was converted to lithium salt by precipitation with a solution of 6% LiClO₄ in acetone.

The chromatography conditions in Source 15Q PE column were optimized so that the peak position of TpT3p was clearly distinguished from that of dTTP. The peaks differ by 4 minutes using the above conditions at 1 ml/min, which exclude the possibility that some contamination of dTTP may have been co-purified with the TpT3p and included in the polymerization assay. This result demonstrates the practical availability of highly purified dinucleotide triphosphates.

20 PCR amplification (step III, Figure 3) included the above described polymerization buffer, additional 2 μ g BSA, 1 μ l of the reaction of step II, 0.1 mM dNTP's, 0.5 pmol T2 template, and 5 pmol of both, T7 and B primers. The reactions, in 20 μ l, were performed in glass capillaries on RapidCycler (Idaho

Technology), using thermal steps of: 1 minute at 94 °C, followed by 30 cycles of 5 seconds at 94 °C, 15 seconds at 50 °C; and 25 seconds at 72 °C. The PCR products were separated on 1.4 % agarose gels, and visualized by UV light following ethidium bromide staining.

- 5 The polymerization assay was also used with Klenow (Exo⁻) DNA polymerase (Fermentas), and Tth DNA polymerase (Promega). Buffer conditions were as recommended by the suppliers. The polymerization assay was performed as described above, but with Klenow step I of the assay differed by incubating the polymerization reaction at 37 °C.

Example 4

Polymerization assay - results

- 10 Incorporation of TpT3p by template-dependent polymerization was tested in a very sensitive assay of three steps, as detailed in Example 3 and Figure 3, and exemplified in Figure 4. In step I, a template containing three (T1-3), four (T1-4) or five (T1-5) runs of deoxyadenosine (A), followed by a non-A containing region was extended from a specific oligonucleotide primer
15 (T7) in the presence of a DNA polymerase and the nucleotide mixtures described in Example 3. In step II, the polymerization products were treated by a single-strand specific exonuclease, so that non-extended single-strand regions in T1 were removed. Only products that were extended in step I, but not digested in step II, could be amplified in step III in the presence of
20 oligonucleotides T7, B and T2. This assay is sensitive enough to identify even a small amount of molecules that were extended in step I, and can be used as a general means to amplify the capacity of polymerases to introduce a nucleotide analog by template extension.

- The results, shown in Figure 4, indicate that PCR-amplification products
25 in step III were obtained when the extension in step I included all the templates in the presence of the four dNTP's. When TpT3p replaced dTTP in the dNTP mixture in step I, there were no PCR products with templates T1-3 and T1-5, but only with template T1-4. This demonstrates that DNA polymerase can incorporate the dinucleotide triphosphate TpT3p only when the template
30 contains an even number of A-runs that match the size and base pairing of the thymidine dinucleotide. DNA sequencing of the PCR products of T1-4 extension confirmed the expected sequence of the template.

 TpT3p concentration that support primer extension, albeit with lower yield, was found to be 50 nM, which is more than 100 fold higher than that

found for dTTP. This suggests affinity differences of the nucleotides to the active site formed by the DNA polymerase, primer and template.

In order to test the possibility that TpT3p inhibits *Exo* VII in Step II of the polymerization assay, and therefore that the ss-DNA regions for subsequent amplification in step III were retained, an additional experiment performed containing the reactants of step I (but without polymerase added), and 3 μ M TpT3p. The absence of any PCR products in both reactions suggests that *Exo* VII is not inhibited in the presence of 3 μ M dinucleotide triphosphates.

These results establish a new concept in enzymatic synthesis of nucleic acids, which opens new avenues for employing polymerases and their substrates in biotechnology.

Example 5

Synthesis and purification of additional di- and trinucleotide triphosphates

Additional dinucleotide triphosphates and one trinucleotide triphosphate were prepared following essentially the same procedures as described above under Examples 1 and 2. These included the triphosphate form of 2'-deoxycytidylyl(3'-5')-2'-deoxyadenosine (CpA3p, SEQ ID NO:89), 2'-deoxycytidylyl(3'-5')-2'-deoxycytidine (CpC3p, SEQ ID NO:90), 2'-deoxyadenylyl(3'-5')-2'-deoxyguanosine (ApG3p, SEQ ID NO:91), thymidylyl(3'-5')-2'-deoxycytidine (TpC3p, SEQ ID NO:14) and thymidylyl-3'-5'-thymidylyl-3'-5'-thymidine (TpTpT3p, SEQ ID NO:80). These compounds were all analyzed by 31 P-NMR giving the expected peak spectra corresponding to the four phosphate groups.

The oligonucleotide triphosphates were purified essentially as described under Example 2 above using a Source 15Q PE column (Pharmacia) and a gradient of 0-40 % ethanol buffered with 50 mM triethylamine bicarbonate (TEAB), pH 7.5-8.0, at flow rate of 1.6 ml/minute (see Table 3 below). The chromatography conditions were optimized to distinguish between the dinucleotides and their corresponding mono-dNTP's so as to eliminate even traces thereof from the preparations.

Table 3

HPLC purification of dinucleotide triphosphates

Nucleotides	Peak position in HPLC (minutes)	Peak absorbance (nm*)
dATP	27.8	261
dCTP	22.5	271
dGTP	25.2	253
TTP	24.3	266
TpT3p	28	266
TpTpT3p	32	266
CpA3p	28.9	263
TpC3p	25.7	268
ApG3p	28.5	255

* - absorbance was measured during the HPLC run in the TEAB/ethanol buffer

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Example 6

Labeled-primer extension assay - methods

The oligonucleotides that were used for this assay are detailed in Table 4 before. The reactions of labeled-primer extension included: polymerization buffer (40 mM Tricine-KOH, pH 8.0; 16 mM KCl; 5 mM MgCl₂ and 4 μg BSA), 1 pmol template, 0.2 pmol of the p201 primer (labeled at its 5' with P³²-γ-ATP using T4 polynucleotide kinase), 1 μM of the indicated dNTP's and 50 μM of the indicated di- or trinucleotide triphosphates in a total volume of 20 μl. The reactions were incubated for 5 minutes at 45 °C, then 5 units of Taq DNA polymerase (see Example 3 for details) were added, followed by 20 minutes at 72 °C. The reactions were terminated with 15 μl of stop solution (95 % formamide, 20 mM EDTA and 0.05% bromophenol blue). Three μl were then separated on Urea-PAGE, and the radiolabeled DNA-bands were detected by phosphoimaging.

Table 4***Oligonucleotides used in the labeled-primer extension assay***

Oligo	Sequence (5' to 3')	SEQ ID NO:
P201	GTAATACGACTCACTATAGG	92
T80	AAAATGTGTGTGCCTATAGTGAGTCGTATTAC	93
T81	AATGAATGAATGCCTATAGTGAGTCGTATTAC	94
T83	GACTGACTCCTATAGTGAGTCGTATTAC	95
T24	TCTGTGTCAAAACCTATAGTGAGTCGTATTAC	96

Example 7***Labeled-primer extension assay - results***

In addition to the above described results (Example 4), incorporation of a variety of dinucleotides by template-dependent polymerization was analyzed using a labeled-primer extension assay, which enabled to clearly visualize and follow the polymerization products (Figures 6, 7 and 8). Templates T80 (SEQ ID NO:97) and T81 (SEQ ID NO:98) were designed to have combinations of GT (SEQ ID NO:99) and AA (SEQ ID NO:100) bases for primer extension, which allow to investigate template-dependent incorporation of the complementary dinucleotides CpA3p and TpT3p, respectively. The results in Figure 6 demonstrate correct incorporation of both dinucleotide triphosphates CpA3p and TpT3p (Figure 6, lanes 3-7), albeit with a lower efficiency as compared to the incorporation of the natural dNTP's (Figure 6, lane 2). The experiment of Figure 7 shows template-dependent incorporation of a mix between a subset of two mononucleotides (dCTP and dATP), and TpT3p (Figure 7, lane 4), or with TpTpT3p (Figure 7, lane 5). In both cases the unnatural building blocks are utilized, but the dinucleotide is incorporated much better than the trinucleotide. In both cases, however, there are traces in the background of polymerization halts in the size of single nucleotides. This seems to be a result of esterase activity of polymerases that is well documented (Canard *et al.*, 1995; Meyer *et al.*, 1998). Incorporation of the dinucleotides CpA3p and CpC3p is compared in Figure 7 (lanes 6 and 7, respectively). Only the complementary dinucleotide (CpA3p) seems to be incorporated by the polymerase, indicating a correct template-dependent synthesis. In Figure 8, two additional dinucleotides, ApC3p and TpC3p, are analyzed for specific incorporation using the template T83 (SEQ ID NO:95). Altogether, four distinct dinucleotide triphosphates and a single trinucleotide triphosphates have

been shown to be incorporated in a template-dependent manner by DNA polymerase, demonstrating a new means to synthesize nucleic acid polymers.

Although the invention has been described in conjunction with specific embodiments thereof, it is evident that many alternatives, modifications and variations will be apparent to those skilled in the art. Accordingly, it is intended to embrace all such alternatives, modifications and variations that fall within the spirit and broad scope of the appended claims. All publications, patents and patent applications mentioned in this specification are herein incorporated in their entirety by reference into the specification, to the same extent as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated herein by reference. In addition, citation or identification of any reference in this application shall not be construed as an admission that such reference is available as prior art to the present invention.

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WHAT IS CLAIMED IS:

1. A novel use of a template-dependent polymerase, the novel use comprising the step of employing said template-dependent polymerase for incorporating at least one oligonucleotide triphosphate onto a nascent oligonucleotide-3'-OH in a template-dependent manner.
2. The novel use of claim 1, wherein said at least one oligonucleotide triphosphate includes at least two mononucleotides.
3. The novel use of claim 1, wherein at least one of said at least one oligonucleotide triphosphate includes a functional group.
4. The novel use of claim 1, wherein at least one of said at least one oligonucleotide triphosphate includes at least one feature selected from the group consisting of at least one nucleotide analog having a sugar analog, at least one nucleotide analog having a base analog and at least one nucleotide analog having an internucleosidyl linkage analog.
5. The novel use of claim 1, wherein said template-dependent polymerase is selected from the group consisting of DNA-dependent DNA polymerase, DNA-dependent RNA polymerase, RNA-dependent DNA polymerase and RNA-dependent RNA polymerase.
6. The novel use of claim 5, wherein said template-dependent polymerase is thermostable.
7. A method of identifying a template-dependent polymerase having increased activity in incorporating oligonucleotide triphosphates onto a nascent oligonucleotide-3'-OH in a template-dependent manner, among a library of mutated template-dependent polymerases, the method comprising the step of screening the library using template-dependent polymerization of oligonucleotide triphosphates for selecting a template-dependent polymerase mutant exhibiting increased activity in incorporating the oligonucleotide triphosphates onto the nascent oligonucleotide-3'-OH in a template-dependent manner.

8. The method of claim 7, further comprising the steps of using said template-dependent polymerase mutant as a basis for creating a second library of mutated template-dependent polymerases derived therefrom and screening the second library using said template-dependent polymerization of oligonucleotide triphosphates for selecting a second template-dependent polymerase mutant demonstrating yet increased activity in incorporating the oligonucleotide triphosphates onto the nascent oligonucleotide-3'-OH in a template-dependent manner.

9. The method of claim 8, wherein said library of mutated template-dependent polymerases is created using at least one method selected from the group of random mutagenesis, random fragments shuffling and gene-family shuffling of genes corresponding to protein fragments and/or domains.

10. A method of assaying a template-dependent polymerase for its activity in incorporating oligonucleotide triphosphates onto a nascent oligonucleotide-3'-OH in a template-dependent manner, the method comprising the step of using template-dependent polymerization of oligonucleotide triphosphates for assaying the template-dependent polymerase for its activity in incorporating oligonucleotide triphosphates onto the nascent oligonucleotide-3'-OH in the template-dependent manner.

11. A method of better exploiting the information transfer capacity of a nucleic acid molecule, the method comprising the step of synthesizing a complementary nucleic acid molecule employing oligonucleotide triphosphates instead of, or in addition to, nucleotide triphosphates, as basic units for synthesis.

12. A method of extending a nascent oligonucleotide-3'-OH in a template-dependent manner, the method comprising the step of contacting the nascent oligonucleotide-3'-OH with a nucleic acid template, a template-dependent polymerase and at least one oligonucleotide triphosphate under conditions in which said nascent oligonucleotide-3'-OH hybridizes with said nucleic acid template and said template-dependent polymerase is active in incorporating said at least one oligonucleotide triphosphate onto a growing 3'-OH group of the nascent oligonucleotide-3'-OH, thereby extending the nascent oligonucleotide-3'-OH in a template-dependent manner.

13. A method of amplifying a nucleic acid template, the method comprising the step of contacting the nucleic acid template with a nascent oligonucleotide-3'-OH, a template-dependent polymerase and at least one oligonucleotide triphosphate under conditions in which said nascent oligonucleotide-3'-OH hybridizes with the nucleic acid template and said template-dependent polymerase is active in incorporating said at least one oligonucleotide triphosphate onto a growing 3'-OH group of said nascent oligonucleotide-3'-OH, thereby amplifying the nucleic acid template.

14. A method of detecting a sequence alteration in a nucleic acid template, the method comprising the step of contacting a nascent oligonucleotide-3'-OH with the nucleic acid template, a template-dependent polymerase and at least one oligonucleotide triphosphate under conditions in which said nascent oligonucleotide-3'-OH hybridizes with said nucleic acid template and said template-dependent polymerase is active in incorporating said at least one oligonucleotide triphosphate onto a growing 3'-OH group of the nascent oligonucleotide-3'-OH, thereby extending the nascent oligonucleotide-3'-OH in a template-dependent manner, said at least one oligonucleotide triphosphate being selected so as to enable extending the nascent oligonucleotide-3'-OH in the template-dependent manner only if the sequence alteration is present, or in the alternative, only if the sequence alteration is absent.

15. A method of detecting the presence or absence of a sequence alteration in a nucleic acid template, the method comprising the steps of:

- (a) contacting the nucleic acid template with a nascent oligonucleotide-3'-OH, a template-dependent polymerase and at least one oligonucleotide triphosphate under conditions in which said nascent oligonucleotide-3'-OH hybridizes with the nucleic acid template and said template-dependent polymerase is active in incorporating said at least one oligonucleotide triphosphate onto a growing 3'-OH group of said nascent oligonucleotide-3'-OH if appropriate base pairing exists between the nucleic acid template and said oligonucleotide triphosphate, and said template-dependent polymerase is substantially inactive in incorporating said at least one oligonucleotide triphosphate onto said growing 3'-OH group of said nascent oligonucleotide-3'-OH if appropriate

18. A method of exponentially amplifying a nucleic acid template, the method comprising the step of contacting the nucleic acid template with a pair of nascent oligonucleotides-3'-OH, said nascent oligonucleotides-3'-OH being hybridizable with opposite strands of the nucleic acid template, a template-dependent polymerase and 4^N oligonucleotide triphosphates each including N monomers, wherein N is an integer greater than 1, under conditions in which said nascent oligonucleotides-3'-OH hybridize with said opposite strands of the nucleic acid template and said template-dependent polymerase is active in incorporating said at least one oligonucleotide triphosphate onto a growing 3'-

OH group of each of said nascent oligonucleotides-3'-OH, thereby exponentially amplifying the nucleic acid template.

19. A method of extending a nascent oligonucleotide-3'-OH in a template-dependent manner, the method comprising the step of contacting the nascent oligonucleotide-3'-OH with a nucleic acid template, a template-dependent polymerase, at least one oligonucleotide triphosphate and at least one nucleotide triphosphate, wherein said at least one oligonucleotide triphosphate and said at least one nucleotide triphosphate are selected such that at least one monomer of said at least one oligonucleotide triphosphate is absent from said at least one nucleotide triphosphate, under conditions in which said nascent oligonucleotide-3'-OH hybridizes with said nucleic acid template and said template-dependent polymerase is active in incorporating said at least one oligonucleotide triphosphate and said at least one nucleotide triphosphate onto a growing 3'-OH of the nascent oligonucleotide-3'-OH, thereby extending the nascent oligonucleotide-3'-OH in a template-dependent manner.

20. A method of amplifying a nucleic acid template, the method comprising the step of contacting the nucleic acid template with a nascent oligonucleotide-3'-OH, a template-dependent polymerase, at least one oligonucleotide triphosphate and at least one nucleotide triphosphate, wherein said at least one oligonucleotide triphosphate and said at least one nucleotide triphosphate are selected such that at least one monomer of said at least one oligonucleotide triphosphate is absent from said at least one nucleotide triphosphate, under conditions in which said nascent oligonucleotide-3'-OH hybridizes with the nucleic acid template and said template-dependent polymerase is active in incorporating said at least one oligonucleotide triphosphate onto a growing 3'-OH group of said nascent oligonucleotide-3'-OH, thereby amplifying the nucleic acid template.

21. A method of detecting a sequence alteration in a nucleic acid template, the method comprising the step of contacting the nascent oligonucleotide-3'-OH with a nucleic acid template, a template-dependent polymerase, at least one oligonucleotide triphosphate and at least one nucleotide triphosphate, wherein said at least one oligonucleotide triphosphate and said at least one nucleotide triphosphate are selected such that at least one monomer of said at least one oligonucleotide triphosphate is absent from said at

23. A method of determining a sequence of a nucleic acid template, the method comprising the steps of:

- (a) contacting in one or more reaction vessels the nucleic acid template with a nascent oligonucleotide-3'-OH, a template-dependent polymerase, 4^N oligonucleotide triphosphates each including N monomers, 4^N oligonucleotide triphosphate analogs each including N monomers of which a 3' monomer includes a chain terminator moiety, wherein N is an integer greater than 1, under conditions in which said nascent oligonucleotide-3'-OH hybridizes with the nucleic acid template and said template-dependent polymerase is active in incorporating said oligonucleotide triphosphates and said oligonucleotide triphosphate analogs onto a growing 3'-OH group of said nascent oligonucleotide-3'-OH, so as to obtain a population of nucleic acid chains each being terminated by a different oligonucleotide triphosphate analog of said 4^N oligonucleotide triphosphate analogs; and
- (b) size separating said population of terminated nucleic acid chains, thereby determining the sequence of the nucleic acid template.

24. The method of claim 23, wherein each of said 4^N oligonucleotide triphosphate analogs is labeled by a unique label.

25. The method of claim 24, wherein at least some of said unique labels is combinatorial labels.

26. A method of engineering functional nucleic acid polymers and polypeptides by introduction of multiple point mutations in nucleic acid sequences, as a novel approach of directed evolution, the method comprising the steps of:

- (a) contacting in reaction vessels a nucleic acid template with a nascent oligonucleotide-3'-OH, a template-dependent polymerase, and 4^N oligonucleotide triphosphates, each including N monomers, wherein N is an integer greater than 1, and wherein at least one of said oligonucleotide triphosphates has a mismatch as compared to the template sequence, under conditions in which the nascent oligonucleotide-3'-OH hybridizes with the nucleic acid template and the template-dependent polymerase is active in incorporating said oligonucleotide triphosphates and said at least

one oligonucleotide triphosphate containing said mismatch onto a growing 3'-OH group of the nascent oligonucleotide-3'-OH, so as to obtain a population of nucleic acid chains each containing one or multiple mutations; and

- (b) amplifying said mutated population of nucleic acid chains and further shuffling, cloning and expressing them by methods known in the art to create pools of degenerate nucleic acid sequences and of degenerate polypeptides; and
- (c) screening said pools for individual clones with desired properties, and then using the selected clones as precursors for additional cycles of degeneration and selection, as described above, until the selected molecules are optimized for the desired function.

27. A method of better exploiting the information transfer and functional capacities of nucleic acid molecules for DNA chip technology and nanotechnology, the method comprising the step of contacting a component selected from at least one nucleic acid template, at least one template-dependent polymerase, at least one nascent oligonucleotide-3'-OH, at least one oligonucleotide triphosphate and/or at least one oligonucleotide triphosphate analog, wherein at least one of said components is attached onto a solid support used in a nanodevice or DNA chip, and wherein said at least one template-dependent polymerase is active in incorporating said at least one oligonucleotide triphosphate and/or said at least one oligonucleotide triphosphate analog onto said growing 3'-OH group of said nascent oligonucleotide-3'-OH, so as to obtain a population of nucleic acid chains bound to the solid support, which can be further manipulated by means as described above including, but not limited to, template-dependent extension, template-dependent amplification, detection of sequence alteration, and detection of nucleic acid sequences.

28. A composition comprising 4^N oligonucleotide triphosphates each having N monomers, wherein N is an integer greater than 1.

29. The composition of claim 28, wherein each of said 4^N oligonucleotide triphosphates includes at least two monomers.

30. The composition of claim 28, wherein at least one of said 4^N oligonucleotide triphosphates includes a functional group.

31. The composition of claim 28, wherein at least one of said 4^N oligonucleotide triphosphates includes at least one feature selected from the group consisting of at least one nucleotide analog having a sugar analog, at least one nucleotide analog having a base analog and at least one nucleotide analog having an internucleosidyl linkage analog.

32. A composition comprising at least one oligonucleotide triphosphate and at least one nucleotide triphosphate, wherein said at least one oligonucleotide triphosphate and said at least one nucleotide triphosphate are selected such that monomers forming said least one oligonucleotide triphosphate are not represented among said at least one nucleotide triphosphate and *vice versa*.

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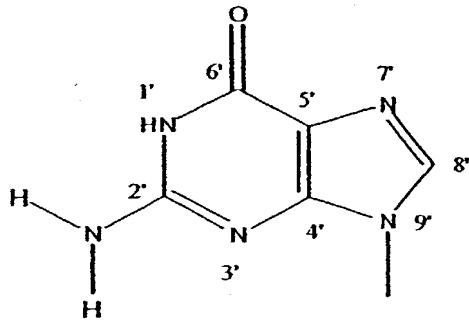
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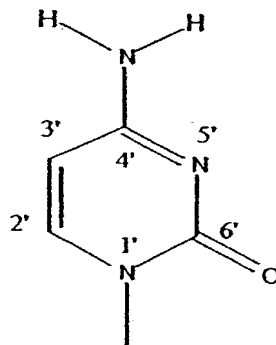
(54) Title: TEMPLATE-DEPENDENT NUCLEIC ACID POLYMERIZATION USING OLIGONUCLEOTIDE TRIPHOS-
PHATES BUILDING BLOCKS

(57) Abstract: A novel use of a template-dependent polymerase. The novel use is effected by employing the template-dependent
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manner.

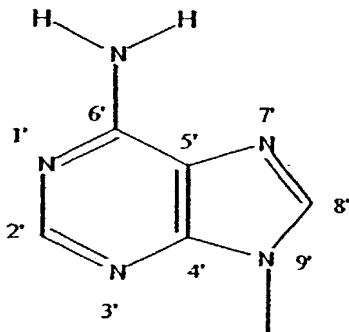
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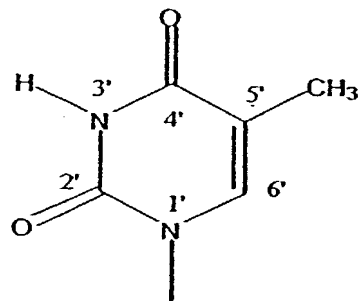
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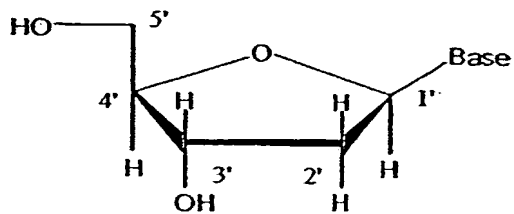
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2'-deoxyadenosine



2'-deoxythymidine



2'-deoxynucleoside

Fig. 1

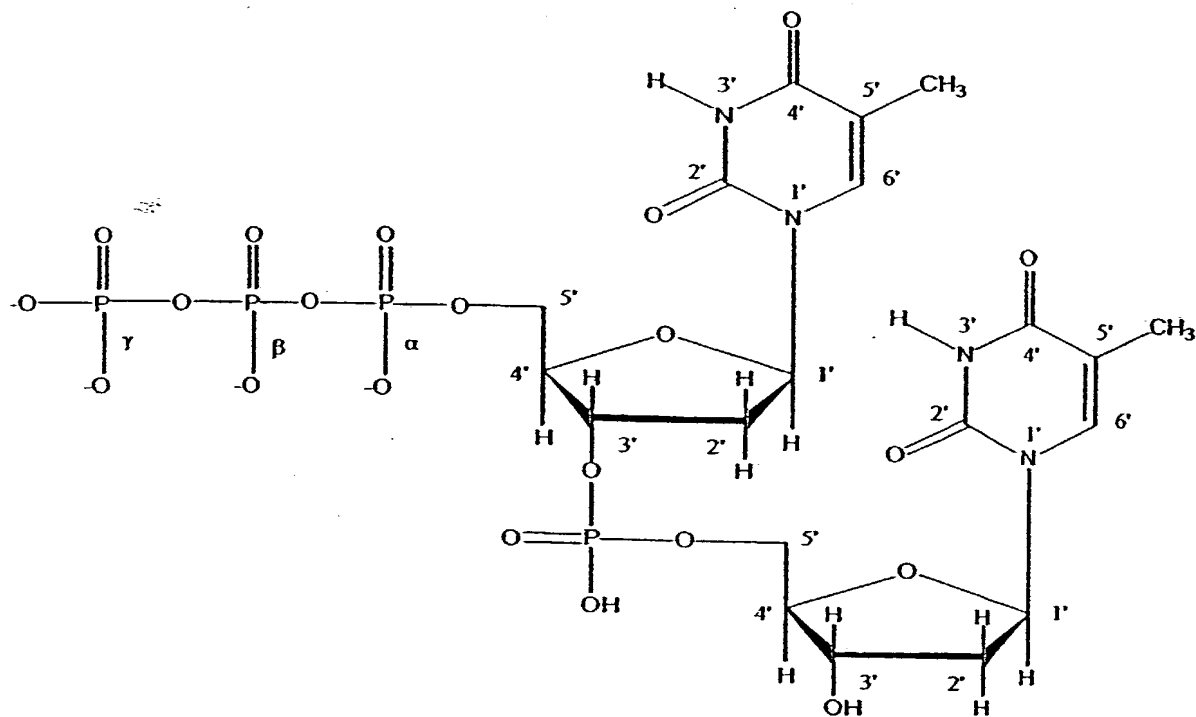
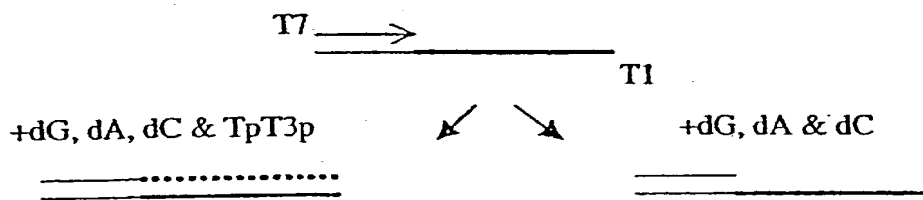


Fig. 2

I. Primer extension



II. Exo VII



III. PCR

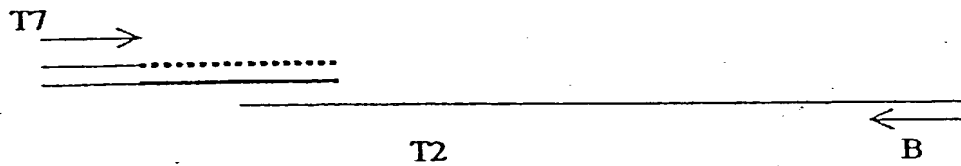
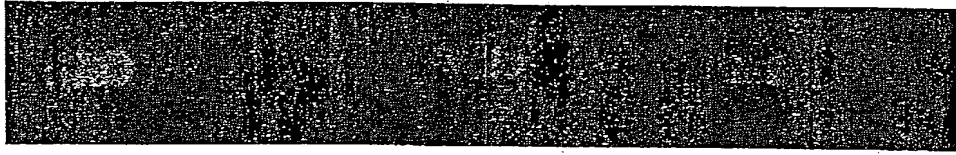
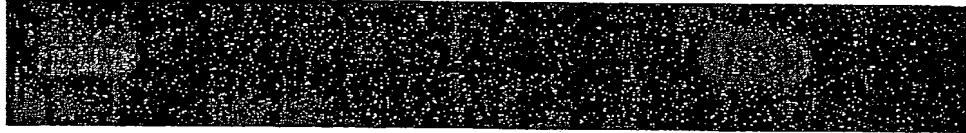


Fig.3

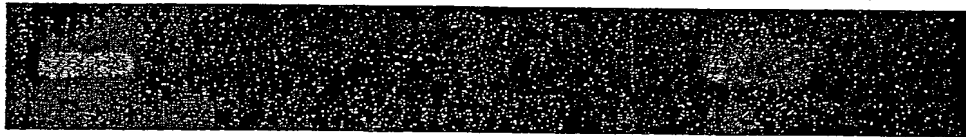
T1-4



T1-3



T1-5



a b c d e f g

Fig. 4

5 / 7

A:

TC GA TT GC TA AG TC CG AT GA TA GC TG AT CG TT CG CT TA
AA

B:

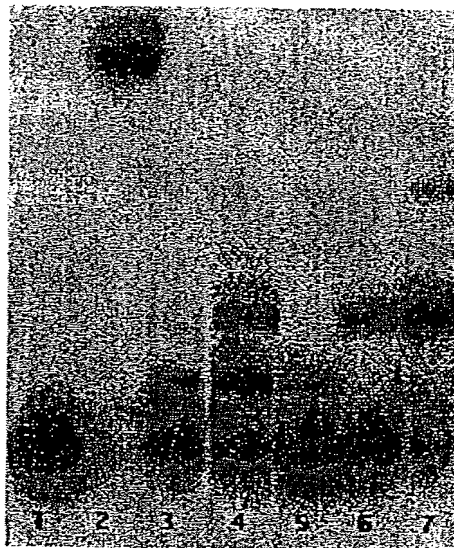
TC GA TT GC TA AG TC CG AT GA TA GC GG AT CG TT CG CT TA
AA

Dinucleotide sets:

set I: AA, **AC**, AG, AT, CG, CT, GA, GC, TA, TC and TT

set II: same, but with CC instead of **AC**.

Fig. 5



P³²-5'-GTAATACGACTCACTATAGG
3'-CATTATGCTGAGTGATATCCGTGTGTGTA AAA (T80)

P³²-5'-GTAATACGACTCACTATAGG
3'-CATTATGCTGAGTGATATCCGTAAGTAAGTAA (T81)

Figure 6:

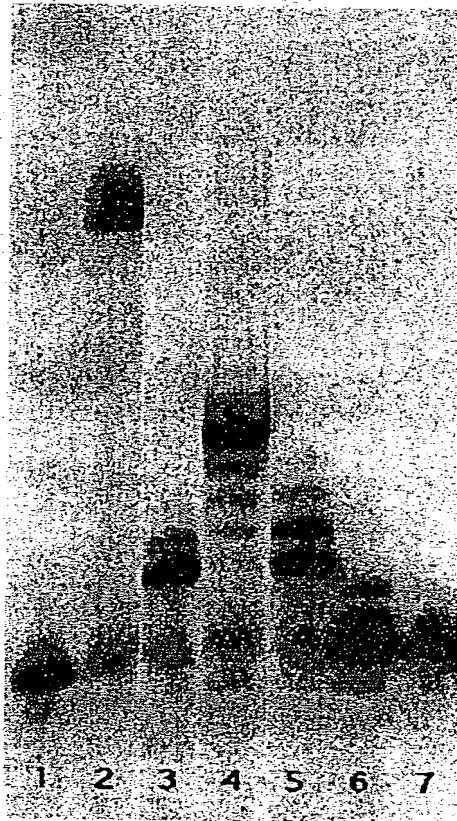


Figure 7:

P^{32} -5'-GTAATACGACTCACTATAGG
3'-CATTATGCTGAGTGATATCCGTGAAAACTGTGTCT (T24)

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Figure 8:

p³²-5'-GTAATACGACTCACTATAGG
3'-CATTATGCTGAGTGATATCCTCAGTCAG (T83)

Docket No.
02/23375

Declaration and Power of Attorney For Patent Application

English Language Declaration

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

TEMPLATE-DEPENDENT NUCLEIC ACID POLYMERIZATION USING OLIGONUCLEOTIDE TRIPHOSPHATES BUILDING BLOCKS

the specification of which



is attached hereto.



was filed on 29 August 2000 as ~~United States Application No.~~ or PCT

International Application Number PCT/IL00/00515

and was amended on _____

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose to the United States Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, Code of federal Regulations, Section 1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, Section 119(a)-(d) or Section 365(b) of any foreign application(s) for patent or inventor's certificate, or Section 365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate or PCT International application having a filing date before that of the application on which priority is claimed.

Prior Foreign Application(s)

Priority Not Claimed

(Number)

(Country)

(Day/Month/Year Filed)



(Number)

(Country)

(Day/Month/Year Filed)



(Number)

(Country)

(Day/Month/Year Filed)



I hereby claim the benefit under 35 U.S.C. Section 119(e) of any United States provisional application(s) listed below:

(Application Serial No.)

(Filing Date)

(Application Serial No.)

(Filing Date)

(Application Serial No.)

(Filing Date)

I hereby claim the benefit under 35 U.S.C. Section 120 of any United States application(s), or Section 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. Section 112. I acknowledge the duty to disclose to the United States Patent and Trademark Office all the information known to me to be material to patentability as defined in Title 37, C.F.R., Section 1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application:

PCT/IL00/00515

29 August 2000

(Application Serial No.)

(Filing Date)

(Status)
(patented, pending, abandoned)

09/387,777

1 September 1999

Abandoned

(Application Serial No.)

(Filing Date)

(Status)
(patented, pending, abandoned)

(Application Serial No.)

(Filing Date)

(Status)
(patented, pending, abandoned)

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith. *(list name and registration number)*

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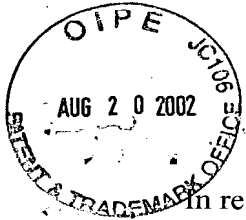
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Anthony Castorina

Tel. No. (703) 415-1581

Fax No. (703) 415- 4864

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Sole or first inventor's signature				Date <u>7.18.02</u>	
Residence	: 14 Moskovitz Street, 76474 Rehovot, Israel	ILX			
Citizenship	: Israeli				
Post Office Address	: 14 Moskovitz Street, 76474 Rehovot, Israel				



10069236 022202 1627
DT05 Rec'd PCT/PTO 20 AUG 2002
#6

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Applicant:

KLESS

Serial No.: 10/069,236

Filed: February __, 2002

For: Template-Dependent Nucleic Acid
Polymerization Using Oligonucleotide
Triphosphates Building Blocks

Examiner:

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AUG 21 2002

TECH CENTER 1600/2900

Group Art Unit:

Attorney

Docket: 02/23375

ASSOCIATE POWER OF ATTORNEY

Director of US Patent and Trademark Office
Washington, D.C. 20231

Sir:

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Sol Sheinbein
Registration No. 25,457
Attorney for Applicant

August 19, 2002

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